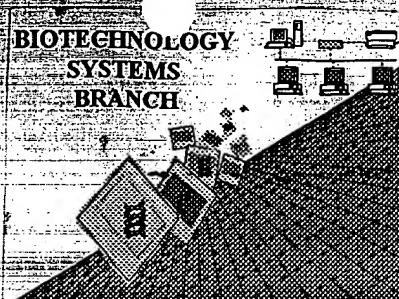


RT-113

## **RAW SEQUENCE LISTING ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#11  
NB  
1/18/01  
72

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/218,913A

Source:

1652

Date Processed by STIC:

1/8/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

1652

RAW SEQUENCE LISTING DATE: 01/08/2001  
PATENT APPLICATION: US/09/218,913A TIME: 15:07:46

Input Set : A:\98,736.Seq.Lst.Rev.txt  
Output Set: N:\CRF3\01082001\I218913A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Hall, Roderick L.  
4 Poll, Christopher T.  
5 Newton, Benjamin B.  
6 Taylor, William J.A.  
8 <120> TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance  
9 <130> FILE REFERENCE: 98,736  
11 <140> CURRENT APPLICATION NUMBER: 09/218,913A  
12 <141> CURRENT FILING DATE: 1998-12-22  
14 <160> NUMBER OF SEQ ID NOS: 71  
16 <170> SOFTWARE: Microsoft Word 97

# ERRORED SEQUENCES

1514 <210> SEQ ID NO: 64  
1515 <211> LENGTH: 20  
1516 <212> TYPE: PRT  
1517 <213> ORGANISM: Homo sapien  
1519 <220> FEATURE:  
1520 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"  
1522 <400> SEQUENCE: 64  
1523 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val  
1524 1 5 10 15  
1526 Val Gly Arg Cys  
E--> 1527 20 20 misaligned amino acid number  
1667 <210> SEQ ID NO: 71  
1668 <211> LENGTH: 225  
1669 <212> TYPE: PRT  
1670 <213> ORGANISM: Homo sapien  
1672 <220> FEATURE:  
1673 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"  
1675 <400> SEQUENCE: 71  
1676 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val  
1677 1 5 10 15  
1679 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr  
1680 20 25 30  
1682 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser  
1683 35 40 45  
1685 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Cys Ala Thr Val  
1686 50 55 60  
1688 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp  
1689 65 70 75 80  
1691 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser  
1692 85 90 95  
1694 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr  
1695 100 105 110  
1697 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg

see next page

## RAW SEQUENCE LISTING

DATE: 01/08/2001

PATENT APPLICATION: US/09/218,913A

TIME: 15:07:47

Input Set : A:\98,736.Seq.Lst.Rev.txt

Output Set: N:\CRF3\01082001\I218913A.raw

```

1698          115          120          125
1700 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
1701          130          135          140
1703 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
1704 145          150          155          160
1706 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
1707          165          170          175
1709 Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
1710          180          185          190
1712 Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
1713          195          200          205
1715 Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
1716          210          215          220
1718 Leu
1719 225
E--> 1726 1

```

*delete at end of file*

*see following page for more error*

## VERIFICATION SUMMARY

DATE: 01/08/2001

PATENT APPLICATION: US/09/218,913A

TIME: 15:07:48

Input Set : A:\98,736.Seq.Lst.Rev.txt

Output Set: N:\CRF3\01082001\I218913A.raw

L:9 M:283 W: Missing Blank Line separator, <130> field identifier  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:426 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:597 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
L:991 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:1098 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47  
L:1205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49  
L:1527 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:64  
L:1726 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:71